

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(1) APPLICANT: Sledziewski Ph.D., Andrzej Z
Bell, Lillian A.
Kindsvogel Ph.D., Wayne R.

(11) TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
FUSIONS

(111) NUMBER OF SEQUENCES: 36

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Seed and Berry
(B) STREET: 6300 Columbia Center
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98104-7092

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.24

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/146,877
(B) FILING DATE: 22-JAN-1988

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/347,291
(B) FILING DATE: 02-MAY-1989

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki J.D., David J.
(B) REGISTRATION NUMBER: 31,392
(C) REFERENCE/DOCKET NUMBER: 990008.446C3

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 206-622-4900
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(C) TELEX: 3723836

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(v) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (D) DEVELOPMENTAL STAGE: Adult
- (F) TISSUE TYPE: Skin
- (G) CELL TYPE: fibroblasts

(vi) IMMEDIATE SOURCE:

- (B) CLONE: pR-rX1

(vii) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 354..3671
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCTCAGCCC	TGCTGCCAG	CACGAGCCTG	TGCTGCCCT	GCCCAACGCA	GACAGCCAGA	60
CCCAGGGCGG	CCCCTCTGGC	GGCTCTGCTC	CTCCCGAAGG	ATGCTTGGGG	AGTGAGGCGA	120
AGCTGGGCGC	TCCTCTCCCC	TACAGCAGCC	CCCTTCCTCC	ATCCCTCTGT	TCTCCTGAGC	180
CTTCAGGAGC	CTGCACCAAGT	CCTGCCTGTC	CTTCTACTCA	GCTGTTACCC	ACTCTGGGAC	240
CAGCAGTCTT	TCTGATAACT	GGGAGAGGGC	AGTAAGGAGG	ACTTCCCTGGA	GGGGGTGACT	300
GTCCAGAGCC	TGGAACTGTG	CCCACACCAAG	AAGCCATCAG	CAGCAAGGAC	ACC ATG	356
				Met		
				1		
CGG CTT CCG GGT GCG ATG CCA GCT CTG GCC CTC AAA GGC GAG CTG CTG	Arg Leu Pro Gly Ala Met Pro Ala Leu Ala Leu Lys	Gly Glu Leu Leu	5	10	15	404
TTG CTG TCT CTC CTG TTA CTT CTG GAA CCA CAG ATC TCT CAG GGC CTG	Leu Leu Ser Leu Leu Leu Leu Glu Pro Gln Ile Ser Gln Gly Leu	20	25	30	452	

GTC GTC ACA CCC CCG GGG CCA GAG CTT GTC CTC AAT GTC TCC AGC ACC Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val Ser Ser Thr 35 40 45	500
TTC GTT CTG ACC TGC TCG GGT TCA GCT CCG GTG GTG TGG GAA CGG ATG Phe Val Leu Thr Cys Ser Gly Ser Ala Pro Val Val Trp Glu Arg Met 50 55 60 65	548
TCC CAG GAG CCC CCA CAG GAA ATG GCC AAG GCC CAG GAT GGC ACC TTC Ser Gin Glu Pro Pro Gln Glu Met Ala Lys Ala Gln Asp Gly Thr Phe 70 75 80	596
TCC AGC GTG CTC ACA CTG ACC AAC CTC ACT GGG CTA GAC ACG GGA GAA Ser Ser Val Leu Thr Leu Thr Asn Leu Thr Gly Leu Asp Thr Gly Glu 85 90 95	644
TAG TTT TGC ACC CAC AAT GAC TCC CGT GGA CTG GAG ACC GAT GAG CGG Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu Thr Asp Glu Arg 100 105 110	692
AAA CGG CTC TAC ATC TTT GTG CCA GAT CCC ACC GTG GGC TTC CTC CCT Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val Gly Phe Leu Pro 115 120 125	740
AAT GAT GCC GAG GAA CTA TTC ATC TTT CTC ACG GAA ATA ACT GAG ATC Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu Ile Thr Glu Ile 130 135 140 145	788
ACC ATT CCA TGC CGA GTA ACA GAC CCA CAG CTG GTG GTG ACA CTG CAC Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val Val Thr Leu His 150 155 160	836
GAG AAG AAA GGG GAC GTT GCA CTG CCT GTC CCC TAT GAT CAC CAA CGT Glu Lys Lys Gly Asp Val Ala Leu Pro Val Pro Tyr Asp His Gln Arg 165 170 175	884
GGC TTT TCT GGT ATC TTT GAG GAC AGA AGC TAC ATC TGC AAA ACC ACC Gly Phe Ser Gly Ile Phe Glu Asp Arg Ser Tyr Ile Cys Lys Thr Thr 180 185 190	932
ATT GGG GAC AGG GAG GTG GAT TCT GAT GCC TAC TAT GTC TAC AGA CTC Ile Gly Asp Arg Glu Val Asp Ser Asp Ala Tyr Tyr Val Tyr Arg Leu 195 200 205	980
CAG GTG TCA TCC ATC AAC GTC TCT GTG AAC GCA GTG CAG ACT GTG GTC Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val Gln Thr Val Val 210 215 220 225	1028
CGC CAG GGT GAG AAC ATC ACC CTC ATG TGC ATT GTG ATC GGG AAT GAG Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile Gly Asn Glu 230 235 240	1076
GTG GTC AAC TTC GAG TGG ACA TAC CCC CGC AAA GAA AGT GGG CGG CTG Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser Gly Arg Leu 245 250 255	1124

GTG GAG CCG GTG ACT GAC TTC CTC TTG GAT ATG CCT TAC CAC ATC CGC Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr His Ile Arg 260 265 270	1172
TCC ATC CTG CAC ATC CCC AGT GCC GAG TTA GAA GAC TCG GGG ACC TAC Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser Gly Thr Tyr 275 280 285	1220
ACC TGC AAT GTG ACG GAG AGT GTG AAT GAC CAT CAG GAT GAA AAG GCC Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp Glu Lys Ala 290 295 300 305	1268
ATC AAC ATC ACC GTG GTT GAG AGC GGC TAC GTG CGG CTC CTG GGA GAG Ile Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu Leu Gly Glu 310 315 320	1316
<u>GTG</u> GGC ACA CTA CAA TTT GCT GAG CTG CAT CGG AGC CGG ACA CTG CAG Val Gly Thr Leu Gln Phe Ala Glu Leu His Arg Ser Arg Thr Leu Gln 325 330 335	1364
GTA GTG TTC GAG GCC TAC CCA CCG CCC ACT GTC CTG TGG TTC AAA GAC Val Val Phe Glu Ala Tyr Pro Pro Thr Val Leu Trp Phe Lys Asp 340 345 350	1412
AAC CGC ACC CTG GGC GAC TCC AGC GCT GGC GAA ATC GCC CTG TCC ACG Asn Arg Thr Leu Gly Asp Ser Ser Ala Gly Glu Ile Ala Leu Ser Thr 355 360 365	1460
CGC AAC GTG TCG GAG ACC CGG TAT GTG TCA GAG CTG ACA CTG GTT CGC Arg Asn Val Ser Glu Thr Arg Tyr Val Ser Glu Leu Thr Leu Val Arg 370 375 380 385	1508
GTG AAG GTG GCA GAG GCT GGC CAC TAC ACC ATG CGG GCC TTC CAT GAG Val Lys Val Ala Glu Ala Gly His Tyr Thr Met Arg Ala Phe His Glu 390 395 400	1556
GAT GCT GAG GTC CAG CTC TCC TTC CAG CTA CAG ATC AAT GTC CCT GTC Asp Ala Glu Val Gln Leu Ser Phe Gln Leu Gln Ile Asn Val Pro Val 405 410 415	1604
CGA GTG CTG GAG CTA AGT GAG AGC CAC CCT GAC AGT GGG GAA CAG ACA Arg Val Leu Glu Leu Ser Glu Ser His Pro Asp Ser Gly Glu Gln Thr 420 425 430	1652
GTC CGC TGT CGT GGC CGG GGC ATG CCC CAG CGG AAC ATC ATC TGG TCT Val Arg Cys Arg Gly Arg Gly Met Pro Gln Pro Asn Ile Ile Trp Ser 435 440 445	1700
GCC TGC AGA GAC CTC AAA AGG TGT CCA CGT GAG CTG CGG CCC ACG CTG Ala Cys Arg Asp Leu Lys Arg Cys Pro Arg Glu Leu Pro Pro Thr Leu 450 455 460 465	1748

CTG GGG AAC AGT TCC GAA GAG GAG AGC CAG CTG GAG ACT AAC GTG ACG Leu Gly Asn Ser Ser Glu Glu Glu Ser Gln Leu Glu Thr Asn Val Thr 470 475 480	1796
TAC TGG GAG GAG GAG CAG GAG TTT GAG GTG GTG AGC ACA CTG CGT CTG Tyr Trp Glu Glu Gln Glu Phe Glu Val Val Ser Thr Leu Arg Leu 485 490 495	1844
CAG CAC GTG GAT CGG CCA CTG TCG GTG CGC TGC ACG CTG CGC AAC GCT Gln His Val Asp Arg Pro Leu Ser Val Arg Cys Thr Leu Arg Asn Ala 500 505 510	1892
GTG GGC CAG GAC ACG CAG GAG GTC ATC GTG GTG CCA CAC TCC TTG CCC Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu Pro 515 520 525	1940
TTF-AAG GTG GTG GTG ATC TCA GCC ATC CTG GCC CTG GTG GTG CTC ACC Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr 530 535 540 545	1988
ATC ATC TCC CTT ATC ATC CTC ATC ATG CTT TGG CAG AAG AAG CCA CGT Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg 550 555 560	2036
TAC GAG ATC CGA TGG AAG GTG ATT GAG TCT GTG AGC TCT GAC GGC CAT Tyr Glu Ile Arg Trp Lys Val Ile Glu Ser Val Ser Ser Asp Gly His 565 570 575	2084
GAG TAC ATC TAC GTG GAC CCC ATG CAG CTG CCC TAT GAC TCC ACG TGG Glu Tyr Ile Tyr Val Asp Pro Met Gln Leu Pro Tyr Asp Ser Thr Trp 580 585 590	2132
GAG CTG CCG CGG GAC CAG CTT GTG CTG GGA CGC ACC CTC GGC TCT GGG Glu Leu Pro Arg Asp Gln Leu Val Leu Gly Arg Thr Leu Gly Ser Gly 595 600 605	2180
GCC TTT GGG CAG GTG GTG GAG GCC ACG GCT CAT GGC CTG AGC CAT TCT Ala Phe Gly Gln Val Val Glu Ala Thr Ala His Gly Leu Ser His Ser 610 615 620 625	2228
CAG GCC ACG ATG AAA GTG GCC GTC AAG ATG CTT AAA TCC ACA GCC CGC Gln Ala Thr Met Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala Arg 630 635 640	2276
AGC AGT GAG AAG CAA GCC CTT ATG TCG GAG CTG AAG ATC ATG AGT CAC Ser Ser Glu Gln Ala Leu Met Ser Glu Leu Lys Ile Met Ser His 645 650 655	2324
CTT GGG CCC CAC CTG AAC GTG GTC AAC CTG TTG GGG GCC TGC ACC AAA Leu Gly Pro His Leu Asn Val Val Asn Leu Leu Gly Ala Cys Thr Lys 660 665 670	2372
GGA GGA CCC ATC TAT ATC ATC ACT GAG TAC TGC CGC TAC GGA GAC CTG Gly Gly Pro Ile Tyr Ile Ile Thr Glu Tyr Cys Arg Tyr Gly Asp Leu 675 680 685	2420

GTG GAC TAC CTG CAC CGC AAC AAA CAC ACC TTC CTG CAG CAC CAC TCC Val Asp Tyr Leu His Arg Asn Lys His Thr Phe Leu Gln His His Ser 690 695 700 705	2468
GAC AAG CGC CGC CCG CCC AGC GCG GAG CTC TAC AGC AAT GCT CTG CCC Asp Lys Arg Arg Pro Pro Ser Ala Glu Leu Tyr Ser Asn Ala Leu Pro 710 715 720	2516
GTT GGG CTC CCC CTG CCC AGC CAT GTG TCC TTG ACC GGG GAG AGC GAC Val Gly Leu Pro Leu Pro Ser His Val Ser Leu Thr Gly Glu Ser Asp 725 730 735	2564
GGT GGC TAC ATG GAC ATG AGC AAG GAC GAG TCG GTG GAC TAT GTG CCC Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Val Asp Tyr Val Pro 740 745 750	2612
ATG CTG GAC ATG AAA GGA GAC GTC AAA TAT GCA GAC ATC GAG TCC TCC Met Leu Asp Met Lys Gly Asp Val Lys Tyr Ala Asp Ile Glu Ser Ser 755 760 765	2660
AAC TAC ATG GCC CCT TAC GAT AAC TAC GTT CCC TCT GCC CCT GAG AGG Asn Tyr Met Ala Pro Tyr Asp Asn Tyr Val Pro Ser Ala Pro Glu Arg 770 775 780 785	2708
ACC TGC CGA GCA ACT TTG ATC AAC GAG TCT CCA GTG CTA AGC TAC ATG Thr Cys Arg Ala Thr Leu Ile Asn Glu Ser Pro Val Leu Ser Tyr Met 790 795 800	2756
GAC CTC GTG GGC TTC AGC TAC CAG GTG GCC AAT GGC ATG GAG TTT CTG Asp Leu Val Gly Phe Ser Tyr Gln Val Ala Asn Gly Met Glu Phe Leu 805 810 815	2804
GCC TCC AAG AAC TGC GTC CAC AGA GAC CTG GCG GCT AGG AAC GTG CTC Ala Ser Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg Asn Val Leu 820 825 830	2852
ATC TGT GAA GGC AAG CTG GTC AAG ATC TGT GAC TTT GGC CTG GCT CGA Ile Cys Glu Gly Lys Leu Val Lys Ile Cys Asp Phe Gly Leu Ala Arg 835 840 845	2900
GAC ATC ATG CGG GAC TCG AAT TAC ATC TCC AAA GGC AGC ACC TTT TTG Asp Ile Met Arg Asp Ser Asn Tyr Ile Ser Lys Gly Ser Thr Phe Leu 850 855 860 865	2948
CCT TTA AAG TGG ATG GCT CCG GAG AGC ATC TTC AAC AGC CTC TAC ACC Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Ser Leu Tyr Thr 870 875 880	2996
ACC CTG AGC GAC GTG TGG TCC TTC GGG ATC CTG CTC TGG GAG ATC TTC Thr Leu Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Phe 885 890 895	3044

ACC TTG GGT GGC ACC CCT TAC CCA GAG CTG CCC ATG AAC GAG CAG TTC Thr Leu Gly Gly Thr Pro Tyr Pro Glu Leu Pro Met Asn Glu Gln Phe 900 905 910	3092
TAC AAT GCC ATC AAA CGG GGT TAC CGC ATG GCC CAG CCT GCC CAT GCC Tyr Asn Ala Ile Lys Arg Gly Tyr Arg Met Ala Gln Pro Ala His Ala 915 920 925	3140
TCC GAC GAG ATC TAT GAG ATC ATG CAG AAG TGC TGG GAA GAG AAG TTT Ser Asp Glu Ile Tyr Glu Ile Met Gln Lys Cys Trp Glu Glu Lys Phe 930 935 940 945	3188
GAG ATT CGG CCC CCC TTC TCC CAG CTG GTG CTG CTT CTC GAG AGA CTG Glu Ile Arg Pro Pro Phe Ser Gln Leu Val Leu Leu Glu Arg Leu 950 955 960	3236
<u>TTG</u> GGC GAA GGT TAC AAA AAG AAG TAC CAG CAG GTG GAT GAG GAG TTT Leu Gly Glu Gly Tyr Lys Lys Tyr Gln Gln Val Asp Glu Glu Phe 965 970 975	3284
CTG AGG AGT GAC CAC CCA GCC ATC CTT CGG TCC CAG GCC CGC TTG CCT Leu Arg Ser Asp His Pro Ala Ile Leu Arg Ser Gln Ala Arg Leu Pro 980 985 990	3332
GGG TTC CAT GGC CTC CGA TCT CCC CTG GAC ACC AGC TCC GTC CTC TAT Gly Phe His Gly Leu Arg Ser Pro Leu Asp Thr Ser Ser Val Leu Tyr 995 1000 1005	3380
ACT GCC GTG CAG CCC AAT GAG GGT GAC AAC GAC TAT ATC ATC CCC CTG Thr Ala Val Gln Pro Asn Glu Gly Asp Asn Asp Tyr Ile Ile Pro Leu 1010 1015 1020 1025	3428
CCT GAC CCC AAA CCC GAG GTT GCT GAC GAG GGC CCA CTG GAG GGT TCC Pro Asp Pro Lys Pro Glu Val Ala Asp Glu Gly Pro Leu Glu Gly Ser 1030 1035 1040	3476
CCC AGC CTA GCC AGC TCC ACC CTG AAT GAA GTC AAC ACC TCC TCA ACC Pro Ser Leu Ala Ser Ser Thr Leu Asn Glu Val Asn Thr Ser Ser Thr 1045 1050 1055	3524
ATC TCC TGT GAC AGC CCC CTG GAG CCC CAG GAC GAA CCA GAG CCA GAG Ile Ser Cys Asp Ser Pro Leu Glu Pro Gln Asp Glu Pro Glu Pro Glu 1060 1065 1070	3572
CCC CAG CTT GAG CTC CAG GTG GAG CCG GAG CCA GAG CTG GAA CAG TTG Pro Gln Leu Glu Leu Gln Val Glu Pro Glu Pro Glu Leu Glu Gln Leu 1075 1080 1085	3620
CCG GAT TCG GGG TGC CCT GCG CCT CGG GCG GAA GCA GAG GAT AGC TTC Pro Asp Ser Gly Cys Pro Ala Pro Arg Ala Glu Ala Glu Asp Ser Phe 1090 1095 1100 1105	3668
CTG TAGGGGGCTG GCCCCTACCC TGCCCTGCCT GAAGCTCCCC CCCTGCCAGC Leu	3721

ACCCAGCATC TCCTGGCCTG GCCTGACCGG GCTTCCTGTC AGCCAGGCTG CCCTTATCAG	3781
CTGTCCCCCTT CTGGAAGCTT TCTGCTCCTG ACGTGTTGTG CCCCCAAACCC TGGGGCTGGC	3841
TTAGGAGGCA AGAAAACCTGC AGGGGCCGTG ACCAGCCCTC TGCCCTCCAGG GAGGCCAACT	3901
GACTCTGAGC CAGGGTTCCC CCAGGGAACT CAGTTTCCC ATATGTAAGA TGGGAAAGTT	3961
AGGCTTGATG ACCCAGAACATC TAGGATTCTC TCCCTGGCTG ACACGGTGGG GAGACCGAAT	4021
CCCTCCCTGG GAAGATTCTT GGAGTTACTG AGGTGGTAAA TTAACATTT TTCTGTTCAG	4081
CCAGCTACCC CTCAAGGAAT CATACTCTC TCCTCGCACT TTTTATCCAC CCAGGAGCTA	4141
GGGAAGAGAC CCTAGCCTCC CTGGCTGCTG GCTGAGCTAG GGCTAGCTT GAGCAGTGT	4201
GCCTCATCCA GAAGAAAGCC AGTCTCCCTCC CTATGATGCC AGTCCCTGCG TTCCCTGGCC	4261
CGAGCTGGTC TGGGGCCATT AGGCAGCCTA ATTAATGCTG GAGGCTGAGC CAAGTACAGG	4321
ACACCCCCAG CCTGCAGCCC TTGCCAGGG CACTGGAGC ACACGCAGCC ATAGCAAGTG	4381
CCTGTGTCCC TGTCTTCAG GCCCATCAGT CCTGGGGCTT TTTCTTTATC ACCCTCAGTC	4441
TTAATCCATC CACCAGAGTC TAGA	4465

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Leu Pro Gly Ala Met Pro Ala Leu Ala Leu Lys Gly Glu Leu	
1 5 10 15	
Leu Leu Leu Ser Leu Leu Leu Leu Glu Pro Gln Ile Ser Gln Gly	
20 25 30	
Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val Ser Ser	
35 40 45	
Thr Phe Val Leu Thr Cys Ser Gly Ser Ala Pro Val Val Trp Glu Arg	
50 55 60	
Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys Ala Gln Asp Gly Thr	
65 70 75 80	

Phe Ser Ser Val Leu Thr Leu Thr Asn Leu Thr Gly Leu Asp Thr Gly
 85 90 95
 Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu Thr Asp Glu
 100 105 110
 Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val Gly Phe Leu
 115 120 125
 Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu Ile Thr Glu
 130 135 140
 Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val Val Thr Leu
 145 150 155 160
 His Glu Lys Lys Gly Asp Val Ala Leu Pro Val Pro Tyr Asp His Gln
 — 165 170 175
 Arg Gly Phe Ser Gly Ile Phe Glu Asp Arg Ser Tyr Ile Cys Lys Thr
 180 185 190
 Thr Ile Gly Asp Arg Glu Val Asp Ser Asp Ala Tyr Tyr Val Tyr Arg
 195 200 205
 Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val Gln Thr Val
 210 215 220
 Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile Gly Asn
 225 230 235 240
 Glu Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser Gly Arg
 245 250 255
 Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr His Ile
 260 265 270
 Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser Gly Thr
 275 280 285
 Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp Glu Lys
 290 295 300
 Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu Leu Gly
 305 310 315 320
 Glu Val Gly Thr Leu Gln Phe Ala Glu Leu His Arg Ser Arg Thr Leu
 325 330 335
 Gln Val Val Phe Glu Ala Tyr Pro Pro Pro Thr Val Leu Trp Phe Lys
 340 345 350
 Asp Asn Arg Thr Leu Gly Asp Ser Ser Ala Gly Glu Ile Ala Leu Ser
 355 360 365

Thr Arg Asn Val Ser Glu Thr Arg Tyr Val Ser Glu Leu Thr Leu Val
370 375 380

Arg Val Lys Val Ala Glu Ala Gly His Tyr Thr Met Arg Ala Phe His
385 390 395 400

Glu Asp Ala Glu Val Gln Leu Ser Phe Gln Leu Gln Ile Asn Val Pro
405 410 415

Val Arg Val Leu Glu Leu Ser Glu Ser His Pro Asp Ser Gly Glu Gln
420 425 430

Thr Val Arg Cys Arg Gly Arg Gly Met Pro Gln Pro Asn Ile Ile Trp
435 440 445

Ser Ala Cys Arg Asp Leu Lys Arg Cys Pro Arg Glu Leu Pro Pro Thr
450 455 460

Leu Leu Gly Asn Ser Ser Glu Glu Glu Ser Gln Leu Glu Thr Asn Val
465 470 475 480

Thr Tyr Trp Glu Glu Gln Glu Phe Glu Val Val Ser Thr Leu Arg
485 490 495

Leu Gln His Val Asp Arg Pro Leu Ser Val Arg Cys Thr Leu Arg Asn
500 505 510

Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu
515 520 525

Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu
530 535 540

Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro
545 550 555 560

Arg Tyr Glu Ile Arg Trp Lys Val Ile Glu Ser Val Ser Ser Asp Gly
565 570 575

His Glu Tyr Ile Tyr Val Asp Pro Met Gln Leu Pro Tyr Asp Ser Thr
580 585 590

Trp Glu Leu Pro Arg Asp Gln Leu Val Leu Gly Arg Thr Leu Gly Ser
595 600 605

Gly Ala Phe Gly Gln Val Val Glu Ala Thr Ala His Gly Leu Ser His
610 615 620

Ser Gln Ala Thr Met Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala
625 630 635 640

Arg Ser Ser Glu Lys Gln Ala Leu Met Ser Glu Leu Lys Ile Met Ser
645 650 655

His Leu Gly Pro His Leu Asn Val Val Asn Leu Leu Gly Ala Cys Thr
660 665 670

Lys Gly Gly Pro Ile Tyr Ile Ile Thr Glu Tyr Cys Arg Tyr Gly Asp
675 680 685

Leu Val Asp Tyr Leu His Arg Asn His Thr Phe Leu Gln His His
690 695 700

Ser Asp Lys Arg Arg Pro Pro Ser Ala Glu Leu Tyr Ser Asn Ala Leu
705 710 715 720

Pro Val Gly Leu Pro Leu Pro Ser His Val Ser Leu Thr Gly Glu Ser
725 730 735

Asp Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Val Asp Tyr Val
740 745 750

Pro Met Leu Asp Met Lys Gly Asp Val Lys Tyr Ala Asp Ile Glu Ser
755 760 765

Ser Asn Tyr Met Ala Pro Tyr Asp Asn Tyr Val Pro Ser Ala Pro Glu
770 775 780

Arg Thr Cys Arg Ala Thr Leu Ile Asn Glu Ser Pro Val Leu Ser Tyr
785 790 795 800

Met Asp Leu Val Gly Phe Ser Tyr Gln Val Ala Asn Gly Met Glu Phe
805 810 815

Leu Ala Ser Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg Asn Val
820 825 830

Leu Ile Cys Glu Gly Lys Leu Val Lys Ile Cys Asp Phe Gly Leu Ala
835 840 845

Arg Asp Ile Met Arg Asp Ser Asn Tyr Ile Ser Lys Gly Ser Thr Phe
850 855 860

Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Ser Leu Tyr
865 870 875 880

Thr Thr Leu Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile
885 890 895

Phe Thr Leu Gly Gly Thr Pro Tyr Pro Glu Leu Pro Met Asn Glu Gln
900 905 910

Phe Tyr Asn Ala Ile Lys Arg Gly Tyr Arg Met Ala Gln Pro Ala His
915 920 925

Ala Ser Asp Glu Ile Tyr Glu Ile Met Gln Lys Cys Trp Glu Glu Lys
930 935 940

Phe Glu Ile Arg Pro Pro Phe Ser Gln Leu Val Leu Leu Leu Glu Arg
 945 950 955 960
 Leu Leu Gly Glu Gly Tyr Lys Lys Tyr Gln Gln Val Asp Glu Glu
 965 970 975
 Phe Leu Arg Ser Asp His Pro Ala Ile Leu Arg Ser Gln Ala Arg Leu
 980 985 990
 Pro Gly Phe His Gly Leu Arg Ser Pro Leu Asp Thr Ser Ser Val Leu
 995 1000 1005
 Tyr Thr Ala Val Gln Pro Asn Glu Gly Asp Asn Asp Tyr Ile Ile Pro
 1010 1015 1020
 Leu Pro Asp Pro Lys Pro Glu Val Ala Asp Glu Gly Pro Leu Glu Gly
 1025 1030 1035 1040
 Ser Pro Ser Leu Ala Ser Ser Thr Leu Asn Glu Val Asn Thr Ser Ser
 1045 1050 1055
 Thr Ile Ser Cys Asp Ser Pro Leu Glu Pro Gln Asp Glu Pro Glu Pro
 1060 1065 1070
 Glu Pro Gln Leu Glu Leu Gln Val Glu Pro Glu Pro Glu Leu Glu Gln
 1075 1080 1085
 Leu Pro Asp Ser Gly Cys Pro Ala Pro Arg Ala Glu Ala Glu Asp Ser
 1090 1095 1100
 Phe Leu
 1105

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATTATACGCT CTCTTCCTCA GGTAATGAG TGCCAGGGCC GGCAAGCCCC CGCTCCA

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGGGGAGCG GGGGCTTGCC GGCCCTGGCA CTCATTTACC TGAGGAAGAG AGAGCT

56

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CATGGGCACG TAATCTATAG ATTATCCTT GCTCATATCC ATGTA

45

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

114

- (ii) MOLECULE TYPE: Other nucleic acid
- (iii) HYPOTHETICAL: N
- (iv) ANTI-SENSE: N
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ZC906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCTGTCCT CTGCTTCAGC CAGAGGTCTT GGGCAGCC

38

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ZC906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCTGTCCT CTGCTTCAGC CAGAGGTCTT GGGCAGCC

38

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ZC1380

115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATGGTGGAA TTCCTGCTGA T

21

(2) INFORMATION FOR SEQ ID NO:9:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

—(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ZC1447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGGTTGTGCA GAGCTGAGGA AGAGATGGA

29

(2) INFORMATION FOR SEQ ID NO:10:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ZC1453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AATTCAATTAT GTTGTGCAA GCCTTCTTGT TCCTGCTAGC TGGTTTCGCT GTTAA

55

116

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC1454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATCTTAACA GCGAAACCAG CTAGCAGGAA CAAGAAGGCT TGCAACAACA TAATG

55

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC1478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATCGCGAGCA TGCAGATCTG A

21

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

117

- (iii) HYPOTHETICAL: N
- (iv) ANTI-SENSE: N
- (vii) IMMEDIATE SOURCE:
(B) CLONE: ZC1479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCTTCAGAT CTGCATGCTG CCGAT

25

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

- (vii) IMMEDIATE SOURCE:
(B) CLONE: ZC1776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGCTGAGCGC AAATGTTGTG TCGAGTGCCC ACCGTGCCA GCTTAGAATT CT

52

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

- (vii) IMMEDIATE SOURCE:
(B) CLONE: ZC1777

118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTAGAGAATT CTAAGCTGGG CACGGTGGC ACTCGACACA ACATTTGCGC TC

52

(2) INFORMATION FOR SEQ ID NO:16:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC1846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCGGCCAC TGTCGGTGCCTG CTGCACGCTG CGCAACGCTG TGGGCCAGGA CACGCAGGAG

60

GTCATCGTGG TGCCACACTC CTTGCCCTTT AAGCA

95

(2) INFORMATION FOR SEQ ID NO:17:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC1847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCTTGCTTA AAGGGCAAGG AGTGTGGCAC CACGATGACC TCCTGCGTGT CCTGGCCCAC

60

AGCGTTGCCAGCAGCAG TGGCC

95

119

(2) INFORMATION FOR SEQ ID NO:18:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC1886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAGTGCCAA GCTTGTCTAG ACTTACCTTT AAAGGGCAAG GAG

43

(2) INFORMATION FOR SEQ ID NO:19:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC1892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCTTGAGCG T

11

(2) INFORMATION FOR SEQ ID NO:20:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

120

- (iii) HYPOTHETICAL: N
- (iv) ANTI-SENSE: N
- (vii) IMMEDIATE SOURCE:
(B) CLONE: ZC1893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTAGACGCTC A

11

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC1894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGCTTCCAGT TCTTCGGCCT CATGTCAGTT CTTCGGCCTC ATGTGAT

47

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC1895

121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTAGATCACA TGAGGCCGAA GAACTGACAT GAGGCCGAAG AACTGGA

47

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
 (B) CLONE: ZC2181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AATTCGGATC CACCATGGGC ACCAGCCACC CGGCCTTCCT GGTGTTAGGC TGCCTGCTGA

60

CCGGCC

66

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
 (B) CLONE: ZC2182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGAGCCTGAT CCTGTGCCAA CTGAGCCTGC CATCGATCCT GCCAAACGAG AACGAGAAGG

60

TTGTGCAGCT A

71

122

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
 (B) CLONE: ZC2183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AATTTAGCTG CACAACCTTC TCGTTCTCGT TTGGCAGGAT CGATGGCAGG CTCAGTTGGC	60
ACAGGATCA	69

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
 (B) CLONE: ZC2184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGCTCAGGCC GGTCAAGCAGG CAGCCTAACCA CCAGGAACGC CGGGTGGCTG GTGCCCATGG	60
TGGATCCG	68

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid

123

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Other nucleic acid

(111) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(v11) IMMEDIATE SOURCE:
(B) CLONE: ZC2311

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGATCACCAT GGCTCAACTG

20

(2) INFORMATION FOR SEQ ID NO:28:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Other nucleic acid

(111) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(v11) IMMEDIATE SOURCE:
(B) CLONE: ZC2351

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGAATTCCAC

10

(2) INFORMATION FOR SEQ ID NO:29:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Other nucleic acid

(111) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

124

(vii) IMMEDIATE SOURCE:
 (B) CLONE: ZC2352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATTATACGCA TGGTGGATT CGAGCT

26

(2) INFORMATION FOR SEQ ID NO:30:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vii) IMMEDIATE SOURCE:
 (B) CLONE: ZC2392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ACGTAAGCTT GTCTAGACTT ACCTTCAGAA CGCAGGGTGG G

41

(2) INFORMATION FOR SEQ ID NO:31:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:
 (B) CLONE: pWK1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ala Leu His Asn His Tyr Thr Glu Lys Ser Leu Ser Leu Ser Pro Gly
 1 5 10 15

Lys

125

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGTGACACTC TCCTGGGAGT TA

22

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCATAGTAGT TACCATATCC TCTTGCACAG

30

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

1240

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACCGAACGTG AGAGGAGTGC TATAA

25

(2) INFORMATION FOR SEQ ID NO:35:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4054 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: p-alpha-17B

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 205..3471
- (D) OTHER INFORMATION:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCCCTGGGGA CGGACCGTGG GCGGGCGGCA GCGGGGGGAC GCGTTTTGGG GACGTGGTGG	60
CCAGCGCCTT CCTGCAGACC CACAGGGAAG TACTCCCTT GACCTCCGGG GAGCTGCGAC	120
CAGGTTATAC GTTGCTGGTG GAAAAGTGAC AATTCTAGGA AAAGAGCTAA AAGCCGGATC	180
GGTGACCGAA AGTTTCCAG AGCT ATG GGG ACT TCC CAT CCG GCG TTC CTG Met Gly Thr Ser His Pro Ala Phe Leu	231
1 5	
GTC TTA GGC TGT CTT CTC ACA GGG CTG AGC CTA ATC CTC TGC CAG CTT Val Leu Gly Cys Leu Leu Thr Gly Leu Ser Leu Ile Leu Cys Gln Leu	279
10 15 20 25	
TCA TTA CCC TCT ATC CTT CCA AAT GAA AAT GAA AAG GTT GTG CAG CTG Ser Leu Pro Ser Ile Leu Pro Asn Glu Asn Glu Lys Val Val Gln Leu	327
30 35 40	
AAT TCA TCC TTT TCT CTG AGA TGC TTT GGG GAG AGT GAA GTG AGC TGG Asn Ser Ser Phe Ser Leu Arg Cys Phe Gly Glu Ser Glu Val Ser Trp	375
45 50 55	

127

CAG TAC CCC ATG TCT GAA GAA GAG AGC TCC GAT GTG GAA ATC AGA AAT	423
Gln Tyr Pro Met Ser Glu Glu Glu Ser Ser Asp Val Glu Ile Arg Asn	
60 65 70	
GAA GAA AAC AAC AGC GGC CTT TTT GTG ACG GTC TTG GAA GTG AGC AGT	471
Glu Glu Asn Asn Ser Gly Leu Phe Val Thr Val Leu Glu Val Ser Ser	
75 80 85	
GCC TCG GCG GCC CAC ACA GGG TTG TAC ACT TGC TAT TAC AAC CAC ACT	519
Ala Ser Ala Ala His Thr Gly Leu Tyr Thr Cys Tyr Tyr Asn His Thr	
90 95 100 105	
CAG ACA GAA GAG AAT GAG CTT GAA GGC AGG CAC ATT TAC ATC TAT GTG	567
Gln Thr Glu Asn Glu Leu Glu Gly Arg His Ile Tyr Ile Tyr Val	
110 115 120	
CCA GAC CCA GAT GTA GCC TTT GTA CCT CTA GGA ATG ACG GAT TAT TTA	615
Pro Asp Pro Asp Val Ala Phe Val Pro Leu Gly Met Thr Asp Tyr Leu	
125 130 135	
GTC ATC GTG GAG GAT GAT GAT TCT GCC ATT ATA CCT TGT CGC ACA ACT	663
Val Ile Val Glu Asp Asp Asp Ser Ala Ile Ile Pro Cys Arg Thr Thr	
140 145 150	
GAT CCC GAG ACT CCT GTA ACC TTA CAC AAC AGT GAG GGG GTG GTA CCT	711
Asp Pro Glu Thr Pro Val Thr Leu His Asn Ser Glu Gly Val Val Pro	
155 160 165	
GCC TCC TAC GAC AGC AGA CAG GGC TTT AAT GGG ACC TTC ACT GTA GGG	759
Ala Ser Tyr Asp Ser Arg Gln Gly Phe Asn Gly Thr Phe Thr Val Gly	
170 175 180 185	
CCC TAT ATC TGT GAG GCC ACC GTC AAA GGA AAG AAG TTC CAG ACC ATC	807
Pro Tyr Ile Cys Glu Ala Thr Val Lys Gly Lys Lys Phe Gln Thr Ile	
190 195 200	
CCA TTT AAT GTT TAT GCT TTA AAA GCA ACA TCA GAG CTG GAT CTA GAA	855
Pro Phe Asn Val Tyr Ala Leu Lys Ala Thr Ser Glu Leu Asp Leu Glu	
205 210 215	
ATG GAA GCT CTT AAA ACC GTG TAT AAG TCA GGG GAA ACG ATT GTG GTC	903
Met Glu Ala Leu Lys Thr Val Tyr Lys Ser Gly Glu Thr Ile Val Val	
220 225 230	
ACC TGT GCT GTT TTT AAC AAT GAG GTG GTT GAC CTT CAA TGG ACT TAC	951
Thr Cys Ala Val Phe Asn Asn Glu Val Val Asp Leu Gln Trp Thr Tyr	
235 240 245	
CCT GGA GAA GTG AAA GGC AAA GGC ATC ACA ATA CTG GAA GAA ATC AAA	999
Pro Gly Glu Val Lys Gly Lys Gly Ile Thr Ile Leu Glu Ile Lys	
250 255 260 265	
GTC CCA TCC ATC AAA TTG GTG TAC ACT TTG ACG GTC CCC GAG GCC ACG	1047
Val Pro Ser Ile Lys Leu Val Tyr Thr Leu Thr Val Pro Glu Ala Thr	
270 275 280	

178

GTG AAA GAC AGT GGA GAT TAC GAA TGT GCT GCC CGC CAG GCT ACC AGG Val Lys Asp Ser Gly Asp Tyr Glu Cys Ala Ala Arg Gln Ala Thr Arg 285 290 295	1095
GAG GTC AAA GAA ATG AAG AAA GTC ACT ATT TCT GTC CAT GAG AAA GGT Glu Val Lys Glu Met Lys Lys Val Thr Ile Ser Val His Glu Lys Gly 300 305 310	1143
TTC ATT GAA ATC AAA CCC ACC TTC AGC CAG TTG GAA GCT GTC AAC CTG Phe Ile Glu Ile Lys Pro Thr Phe Ser Gln Leu Glu Ala Val Asn Leu 315 320 325	1191
CAT GAA GTC AAA CAT TTT GTT GTA GAG GTG CGG GCC TAC CCA CCT CCC His Glu Val Lys His Phe Val Val Glu Val Arg Ala Tyr Pro Pro Pro 330 335 340 345	1239
AGG ATA TCC TGG CTG AAA AAC AAT CTG ACT CTG ATT GAA AAT CTC ACT Arg Ile Ser Trp Leu Lys Asn Asn Leu Thr Leu Ile Glu Asn Leu Thr 350 355 360	1287
GAG ATC ACC ACT GAT GTG GAA AAG ATT CAG GAA ATA AGG TAT CGA AGC Glu Ile Thr Thr Asp Val Glu Lys Ile Gln Glu Ile Arg Tyr Arg Ser 365 370 375	1335
AAA TTA AAG CTG ATC CGT GCT AAG GAA GAC AGT GGC CAT TAT ACT Lys Leu Lys Leu Ile Arg Ala Lys Glu Glu Asp Ser Gly His Tyr Thr 380 385 390	1383
ATT GTA GCT CAA AAT GAA GAT GCT GTG AAG AGC TAT ACT TTT GAA CTG Ile Val Ala Gln Asn Glu Asp Ala Val Lys Ser Tyr Thr Phe Glu Leu 395 400 405	1431
TTA ACT CAA GTT CCT TCA TCC ATT CTG GAC TTG GTC GAT GAT CAC CAT Leu Thr Gln Val Pro Ser Ser Ile Leu Asp Leu Val Asp Asp His His 410 415 420 425	1479
GGC TCA ACT GGG GGA CAG ACG GTG AGG TGC ACA GCT GAA GGC ACG CCG Gly Ser Thr Gly Gly Gln Thr Val Arg Cys Thr Ala Glu Gly Thr Pro 430 435 440	1527
CTT CCT GAT ATT GAG TGG ATG ATA TGC AAA GAT ATT AAG AAA TGT AAT Leu Pro Asp Ile Glu Trp Met Ile Cys Lys Asp Ile Lys Lys Cys Asn 445 450 455	1575
AAT GAA ACT TCC TGG ACT ATT TTG GCC AAC AAT GTC TCA AAC ATC ATC Asn Glu Thr Ser Trp Thr Ile Leu Ala Asn Asn Val Ser Asn Ile Ile 460 465 470	1623
ACG GAG ATC CAC TCC CGA GAC AGG AGT ACC GTG GAG GGC CGT GTG ACT Thr Glu Ile His Ser Arg Asp Arg Ser Thr Val Glu Gly Arg Val Thr 475 480 485	1671

TTC	GCC	AAA	GTG	GAG	GAG	ACC	ATC	GCC	GTG	CGA	TGC	CTG	GCT	AAG	AAT	1719
Phe	Ala	Lys	Val	Glu	Glu	Thr	Ile	Ala	Val	Arg	Cys	Leu	Ala	Lys	Asn	
490				495					500					505		
CTC	CTT	GGA	GCT	GAG	AAC	CGA	GAG	CTG	AAG	CTG	GTG	GCT	CCC	ACC	CTG	1767
Leu	Leu	Gly	Ala	Glu	Asn	Arg	Glu	Leu	Lys	Leu	Val	Ala	Pro	Thr	Leu	
				510					515					520		
CGT	TCT	GAA	CTC	ACG	GTG	GCT	GCT	GCA	GTC	CTG	GTG	CTG	TTG	GTG	ATT	1815
Arg	Ser	Glu	Leu	Thr	Val	Ala	Ala	Ala	Val	Leu	Val	Leu	Leu	Val	Ile	
				525					530					535		
GTG	ATC	ATC	TCA	CTT	ATT	GTC	CTG	GTT	GTC	ATT	TGG	AAA	CAG	AAA	CCG	1863
Val	Ile	Ile	Ser	Leu	Ile	Val	Leu	Val	Val	Ile	Trp	Lys	Gln	Lys	Pro	
				540					545			550				
AGG	TAT	GAA	ATT	CCG	TGG	AGG	GTC	ATT	GAA	TCA	ATC	AGC	CCG	GAT	GGA	1911
Arg	Tyr	Glu	Ile	Arg	Trp	Arg	Val	Ile	Glu	Ser	Ile	Ser	Pro	Asp	Gly	
				555					560			565				
CAT	GAA	TAT	ATT	TAT	GTG	GAC	CCG	ATG	CAG	CTG	CCT	TAT	GAC	TCA	AGA	1959
His	Glu	Tyr	Ile	Tyr	Val	Asp	Pro	Met	Gln	Leu	Pro	Tyr	Asp	Ser	Arg	
				570					575			580			585	
TGG	GAG	TTT	CCA	AGA	GAT	GGA	CTA	GTG	CTT	GGT	CGG	GTC	TTG	GGG	TCT	2007
Trp	Glu	Phe	Pro	Arg	Asp	Gly	Leu	Val	Leu	Gly	Arg	Val	Leu	Gly	Ser	
				590					595			600				
GGA	GCG	TTT	GGG	AAG	GTG	GTT	GAA	GGA	ACA	GCC	TAT	GGA	TTA	AGC	CGG	2055
Gly	Ala	Phe	Gly	Lys	Val	Val	Glu	Gly	Thr	Ala	Tyr	Gly	Leu	Ser	Arg	
				605					610			615				
TCC	CAA	CCT	GTC	ATG	AAA	GTT	GCA	GTG	AAG	ATG	CTA	AAA	CCC	ACG	GCC	2103
Ser	Gln	Pro	Val	Met	Lys	Val	Ala	Val	Lys	Met	Leu	Lys	Pro	Thr	Ala	
				620					625			630				
AGA	TCC	AGT	GAA	AAA	CAA	GCT	CTC	ATG	TCT	GAA	CTG	AAG	ATA	ATG	ACT	2151
Arg	Ser	Ser	Glu	Lys	Gln	Ala	Leu	Met	Ser	Glu	Leu	Lys	Ile	Met	Thr	
				635					640			645				
CAC	CTG	GGG	CCA	CAT	TTG	AAC	ATT	GTA	AAC	TTG	CTG	GGA	GCC	TGC	ACC	2199
His	Leu	Gly	Pro	His	Leu	Asn	Ile	Val	Asn	Leu	Leu	Gly	Ala	Cys	Thr	
				650					655			660			665	
AAG	TCA	GGC	CCC	ATT	TAC	ATC	ATC	ACA	GAG	TAT	TGC	TTC	TAT	GGA	GAT	2247
Lys	Ser	Gly	Pro	Ile	Tyr	Ile	Ile	Thr	Glu	Tyr	Cys	Phe	Tyr	Gly	Asp	
				670					675			680				
TTG	GTC	AAC	TAT	TTG	CAT	AAG	AAT	AGG	GAT	AGC	TTC	CTG	AGC	CAC	CAC	2295
Leu	Val	Asn	Tyr	Leu	His	Lys	Asn	Arg	Asp	Ser	Phe	Leu	Ser	His	His	
				685					690			695				
CCA	GAG	AAG	CCA	AAG	AAA	GAG	CTG	GAT	ATC	TTT	GGA	TTG	AAC	CCT	GCT	2343
Pro	Glu	Lys	Pro	Lys	Lys	Glu	Leu	Asp	Ile	Phe	Gly	Leu	Asn	Pro	Ala	
				700					705			710				

GAT GAA AGC ACA CGG AGC TAT GTT ATT TTA TCT TTT GAA AAC AAT GGT Asp Glu Ser Thr Arg Ser Tyr Val Ile Leu Ser Phe Glu Asn Asn Gly 715 720 725	2391
GAC TAC ATG GAC ATG AAG CAG GCT GAT ACT ACA CAG TAT GTC CCC ATG Asp Tyr Met Asp Met Lys Gln Ala Asp Thr Thr Gln Tyr Val Pro Met 730 735 740 745	2439
CTA GAA AGG AAA GAG GTT TCT AAA TAT TCC GAC ATC CAG AGA TCA CTC Leu Glu Arg Lys Glu Val Ser Lys Tyr Ser Asp Ile Gln Arg Ser Leu 750 755 760	2487
TAT GAT CGT CCA GCC TCA TAT AAG AAG AAA TCT ATG TTA GAC TCA GAA Tyr Asp Arg Pro Ala Ser Tyr Lys Lys Ser Met Leu Asp Ser Glu 765 770 775	2535
GTC AAA AAC CTC CTT TCA GAT GAT AAC TCA GAA GGC CTT ACT TTA TTG Val Lys Asn Leu Leu Ser Asp Asp Asn Ser Glu Gln Leu Thr Leu Leu 780 785 790	2583
GAT TTG TTG AGC TTC ACC TAT CAA GTT GCC CGA GGA ATG GAG TTT TTG Asp Leu Leu Ser Phe Thr Tyr Gln Val Ala Arg Gln Met Glu Phe Leu 795 800 805	2631
GCT TCA AAA AAT TGT GTC CAC CGT GAT CTG GCT GCT CGC AAC GTC CTC Ala Ser Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg Asn Val Leu 810 815 820 825	2679
CTG GCA CAA GGA AAA ATT GTG AAG ATC TGT GAC TTT GGC CTG GCC AGA Leu Ala Gln Gly Lys Ile Val Lys Ile Cys Asp Phe Gly Leu Ala Arg 830 835 840	2727
GAC ATC ATG CAT GAT TCG AAC TAT GTG TCG AAA GGC AGT ACC TTT CTG Asp Ile Met His Asp Ser Asn Tyr Val Ser Lys Gln Ser Thr Phe Leu 845 850 855	2775
CCC GTG AAG TGG ATG GCT CCT GAG AGC ATC TTT GAC AAC CTC TAC ACC Pro Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asp Asn Leu Tyr Thr 860 865 870	2823
ACA CTG AGT GAT GTC TGG TCT TAT GGC ATT CTG CTC TGG GAG ATC TTT Thr Leu Ser Asp Val Trp Ser Tyr Gln Ile Leu Leu Trp Glu Ile Phe 875 880 885	2871
TCC CTT GGT GGC ACC CCT TAC CCC GGC ATG ATG GTG GAT TCT ACT TTC Ser Leu Gln Gly Thr Pro Tyr Pro Gln Met Met Val Asp Ser Thr Phe 890 895 900 905	2919
TAC AAT AAG ATC AAG AGT GGG TAC CGG ATG GCC AAG CCT GAC CAC GCT Tyr Asn Lys Ile Lys Ser Gln Tyr Arg Met Ala Lys Pro Asp His Ala 910 915 920	2967

ACC AGT GAA GTC TAC GAG ATC ATG GTG AAA TGC TGG AAC AGT GAG CCG Thr Ser Glu Val Tyr Glu Ile Met Val Lys Cys Trp Asn Ser Glu Pro 925 930 935	3015
GAG AAG AGA CCC TCC TTT TAC CAC CTG AGT GAG ATT GTG GAG AAT CTG Glu Lys Arg Pro Ser Phe Tyr His Leu Ser Glu Ile Val Glu Asn Leu 940 945 950	3063
CTG CCT GGA CAA TAT AAA AAG AGT TAT GAA AAA ATT CAC CTG GAC TTC Leu Pro Gly Gln Tyr Lys Lys Ser Tyr Glu Lys Ile His Leu Asp Phe 955 960 965	3111
CTG AAG AGT GAC CAT CCT GCT GTG GCA CGC ATG CGT GTG GAC TCA GAC Leu Lys Ser Asp His Pro Ala Val Ala Arg Met Arg Val Asp Ser Asp 970 975 980 985	3159
<u>AAT</u> GCA TAC ATT GGT GTC ACC TAC AAA AAC GAG GAA GAC AAG CTG AAG Asn Ala Tyr Ile Gly Val Thr Tyr Lys Asn Glu Glu Asp Lys Leu Lys 990 995 1000	3207
GAC TGG GAG GGT GGT CTG GAT GAG CAG AGA CTG AGC GCT GAC AGT GGC Asp Trp Glu Gly Leu Asp Glu Gln Arg Leu Ser Ala Asp Ser Gly 1005 1010 1015	3255
TAC ATC ATT CCT CTG CCT GAC ATT GAC CCT GTC CCT GAG GAG GAG GAC Tyr Ile Ile Pro Leu Pro Asp Ile Asp Pro Val Pro Glu Glu Glu Asp 1020 1025 1030	3303
CTG GGC AAG AGG AAC AGA CAC AGC TCG CAG ACC TCT GAA GAG AGT GCC Leu Gly Lys Arg Asn Arg His Ser Ser Gln Thr Ser Glu Glu Ser Ala 1035 1040 1045	3351
ATT GAG ACG GGT TCC AGC AGT TCC ACC TTC ATC AAG AGA GAG GAC GAG Ile Glu Thr Gly Ser Ser Ser Ser Thr Phe Ile Lys Arg Glu Asp Glu 1050 1055 1060 1065	3399
ACC ATT GAA GAC ATC GAC ATG ATG GAC GAC ATC GGC ATA GAC TCT TCA Thr Ile Glu Asp Ile Asp Met Met Asp Asp Ile Gly Ile Asp Ser Ser 1070 1075 1080	3447
GAC CTG GTG GAA GAC AGC TTC CTG TAACTGGCGG ATT CGAGGGG TTCC TTCCAC Asp Leu Val Glu Asp Ser Phe Leu 1085	3501
TTCTGGGCC ACCTCTGGAT CCCGTTCAAGA AAACCACTTT ATT GCAATGC GGAGGTTGAG	3561
AGGAGGACTT GGTTGATGTT TAAAGAGAAG TTCCCAGCCA AGGGCCTCGG GGAGCGTTCT	3621
AAATATGAAT GAATGGATA TTTTGAATG AAC TTTGTCA GTGTTGCCCT TTGCAATGCC	3681
TCAGTAGCAT CTCAGTGGTG TGTGAAGTTT GGAGATAGAT GGATAAGGGA ATAATAGGCC	3741
ACAGAAGGTG AACTTTGTGC TTCAAGGACA TTGGTGAGAG TCCAACAGAC ACAATTATA	3801
CTGCGACAGA ACTTCAGCAT TGTAATTATG TAAATAACTC TAACCAAGGC TGTGTTAGA	3861

TTGTATTAAC TATCTTCTTT GGACTTCTGA AGAGACCACT CAATCCATCC TGTACTTCCC	3921
TCTTGAAACC TGATGTAGCT GCTGTTGAAC TTTTAAAGA AGTGCATGAA AAACCATTTC	3981
TGAACCTTAA AAGGTACTGG TACTATAGCA TTTGCTATC TTTTTAGTG TTAAAGAGAT	4041
AAAGAATAAT AAG	4054

(2) INFORMATION FOR SEQ ID NO:36:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1089 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Gly Thr Ser His Pro Ala Phe Leu Val Leu Gly Cys Leu Leu Thr	
1 5 10 15	
Gly Leu Ser Leu Ile Leu Cys Gln Leu Ser Leu Pro Ser Ile Leu Pro	
20 25 30	
Asn Glu Asn Glu Lys Val Val Gln Leu Asn Ser Ser Phe Ser Leu Arg	
35 40 45	
Cys Phe Gly Glu Ser Glu Val Ser Trp Gln Tyr Pro Met Ser Glu Glu	
50 55 60	
Glu Ser Ser Asp Val Glu Ile Arg Asn Glu Glu Asn Asn Ser Gly Leu	
65 70 75 80	
Phe Val Thr Val Leu Glu Val Ser Ser Ala Ser Ala Ala His Thr Gly	
85 90 95	
Leu Tyr Thr Cys Tyr Tyr Asn His Thr Gln Thr Glu Glu Asn Glu Leu	
100 105 110	
Glu Gly Arg His Ile Tyr Ile Tyr Val Pro Asp Pro Asp Val Ala Phe	
115 120 125	
Val Pro Leu Gly Met Thr Asp Tyr Leu Val Ile Val Glu Asp Asp Asp	
130 135 140	
Ser Ala Ile Ile Pro Cys Arg Thr Thr Asp Pro Glu Thr Pro Val Thr	
145 150 155 160	
Leu His Asn Ser Glu Gly Val Val Pro Ala Ser Tyr Asp Ser Arg Gln	
165 170 175	

Gly Phe Asn Gly Thr Phe Thr Val Gly Pro Tyr Ile Cys Glu Ala Thr
 180 185 190
 Val Lys Gly Lys Lys Phe Gln Thr Ile Pro Phe Asn Val Tyr Ala Leu
 195 200 205
 Lys Ala Thr Ser Glu Leu Asp Leu Glu Met Glu Ala Leu Lys Thr Val
 210 215 220
 Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys Ala Val Phe Asn Asn
 225 230 235 240
 Glu Val Val Asp Leu Gln Trp Thr Tyr Pro Gly Glu Val Lys Gly Lys
 245 250 255
 Gly Ile Thr Ile Leu Glu Glu Ile Lys Val Pro Ser Ile Lys Leu Val
 260 265 270
 Tyr Thr Leu Thr Val Pro Glu Ala Thr Val Lys Asp Ser Gly Asp Tyr
 275 280 285
 Glu Cys Ala Ala Arg Gln Ala Thr Arg Glu Val Lys Glu Met Lys Lys
 290 295 300
 Val Thr Ile Ser Val His Glu Lys Gly Phe Ile Glu Ile Lys Pro Thr
 305 310 315 320
 Phe Ser Gln Leu Glu Ala Val Asn Leu His Glu Val Lys His Phe Val
 325 330 335
 Val Glu Val Arg Ala Tyr Pro Pro Pro Arg Ile Ser Trp Leu Lys Asn
 340 345 350
 Asn Leu Thr Leu Ile Glu Asn Leu Thr Glu Ile Thr Thr Asp Val Glu
 355 360 365
 Lys Ile Gln Glu Ile Arg Tyr Arg Ser Lys Leu Lys Leu Ile Arg Ala
 370 375 380
 Lys Glu Glu Asp Ser Gly His Tyr Thr Ile Val Ala Gln Asn Glu Asp
 385 390 395 400
 Ala Val Lys Ser Tyr Thr Phe Glu Leu Leu Thr Gln Val Pro Ser Ser
 405 410 415
 Ile Leu Asp Leu Val Asp Asp His His Gly Ser Thr Gly Gly Gln Thr
 420 425 430
 Val Arg Cys Thr Ala Glu Gly Thr Pro Leu Pro Asp Ile Glu Trp Met
 435 440 445
 Ile Cys Lys Asp Ile Lys Lys Cys Asn Asn Glu Thr Ser Trp Thr Ile
 450 455 460

134

Leu Ala Asn Asn Val Ser Asn Ile Ile Thr Glu Ile His Ser Arg Asp
 465 470 475 480

Arg Ser Thr Val Glu Gly Arg Val Thr Phe Ala Lys Val Glu Glu Thr
 485 490 495

Ile Ala Val Arg Cys Leu Ala Lys Asn Leu Leu Gly Ala Glu Asn Arg
 500 505 510

Glu Leu Lys Leu Val Ala Pro Thr Leu Arg Ser Glu Leu Thr Val Ala
 515 520 525

Ala Ala Val Leu Val Leu Val Ile Val Ile Ile Ser Leu Ile Val
 530 535 540

Leu Val Val Ile Trp Lys Gln Lys Pro Arg Tyr Glu Ile Arg Trp Arg
545 550 555 560

Val Ile Glu Ser Ile Ser Pro Asp Gly His Glu Tyr Ile Tyr Val Asp
 565 570 575

Pro Met Gln Leu Pro Tyr Asp Ser Arg Trp Glu Phe Pro Arg Asp Gly
 580 585 590

Leu Val Leu Gly Arg Val Leu Gly Ser Gly Ala Phe Gly Lys Val Val
 595 600 605

Glu Gly Thr Ala Tyr Gly Leu Ser Arg Ser Gln Pro Val Met Lys Val
 610 615 620

Ala Val Lys Met Leu Lys Pro Thr Ala Arg Ser Ser Glu Lys Gln Ala
 625 630 635 640

Leu Met Ser Glu Leu Lys Ile Met Thr His Leu Gly Pro His Leu Asn
 645 650 655

Ile Val Asn Leu Leu Gly Ala Cys Thr Lys Ser Gly Pro Ile Tyr Ile
 660 665 670

Ile Thr Glu Tyr Cys Phe Tyr Gly Asp Leu Val Asn Tyr Leu His Lys
 675 680 685

Asn Arg Asp Ser Phe Leu Ser His His Pro Glu Lys Pro Lys Lys Glu
 690 695 700

Leu Asp Ile Phe Gly Leu Asn Pro Ala Asp Glu Ser Thr Arg Ser Tyr
 705 710 715 720

Val Ile Leu Ser Phe Glu Asn Asn Gly Asp Tyr Met Asp Met Lys Gln
 725 730 735

Ala Asp Thr Thr Gln Tyr Val Pro Met Leu Glu Arg Lys Glu Val Ser
 740 745 750

135

Lys Tyr Ser Asp Ile Gln Arg Ser Leu Tyr Asp Arg Pro Ala Ser Tyr
 755 760 765
 Lys Lys Lys Ser Met Leu Asp Ser Glu Val Lys Asn Leu Leu Ser Asp
 770 775 780
 Asp Asn Ser Glu Gly Leu Thr Leu Leu Asp Leu Leu Ser Phe Thr Tyr
 785 790 795 800
 Gln Val Ala Arg Gly Met Glu Phe Leu Ala Ser Lys Asn Cys Val His
 805 810 815
 Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Ala Gln Gly Lys Ile Val
 820 825 830
 Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Met His Asp Ser Asn
 — 835 840 845
 Tyr Val Ser Lys Gly Ser Thr Phe Leu Pro Val Lys Trp Met Ala Pro
 850 855 860
 Glu Ser Ile Phe Asp Asn Leu Tyr Thr Leu Ser Asp Val Trp Ser
 865 870 875 880
 Tyr Gly Ile Leu Leu Trp Glu Ile Phe Ser Leu Gly Gly Thr Pro Tyr
 885 890 895
 Pro Gly Met Met Val Asp Ser Thr Phe Tyr Asn Lys Ile Lys Ser Gly
 900 905 910
 Tyr Arg Met Ala Lys Pro Asp His Ala Thr Ser Glu Val Tyr Glu Ile
 915 920 925
 Met Val Lys Cys Trp Asn Ser Glu Pro Glu Lys Arg Pro Ser Phe Tyr
 930 935 940
 His Leu Ser Glu Ile Val Glu Asn Leu Leu Pro Gly Gln Tyr Lys Lys
 945 950 955 960
 Ser Tyr Glu Lys Ile His Leu Asp Phe Leu Lys Ser Asp His Pro Ala
 965 970 975
 Val Ala Arg Met Arg Val Asp Ser Asp Asn Ala Tyr Ile Gly Val Thr
 980 985 990
 Tyr Lys Asn Glu Glu Asp Lys Leu Lys Asp Trp Glu Gly Gly Leu Asp
 995 1000 1005
 Glu Gln Arg Leu Ser Ala Asp Ser Gly Tyr Ile Ile Pro Leu Pro Asp
 1010 1015 1020
 Ile Asp Pro Val Pro Glu Glu Asp Leu Gly Lys Arg Asn Arg His
 1025 1030 1035 1040

Ser Ser Gln Thr Ser Glu Glu Ser Ala Ile Glu Thr Gly Ser Ser Ser
1045 1050 1055

Ser Thr Phe Ile Lys Arg Glu Asp Glu Thr Ile Glu Asp Ile Asp Met
1060 1065 1070

Met Asp Asp Ile Gly Ile Asp Ser Ser Asp Leu Val Glu Asp Ser Phe
1075 1080 1085

Leu